

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 16:32:24 ; Search time 68 Seconds
(without alignments)
2047.955 Million cell updates/sec

Title: us-09-635-501-2

Perfect score: 4291

Sequence: 1 MSSSSWLLLSLVAVTAAQST.....ISKGNPNPGFQNTDDVQTSF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	4291	100.0	805	4	Q9NRA7	Q9Nra7 homo sapien
2	4288	99.9	805	4	Q9BYF1	Q9byf1 homo sapien
3	4281	99.8	804	4	Q9UF26	Q9uf26 homo sapien
4	3485	81.2	798	11	Q99N71	Q99n71 mus musculus
5	1539	35.9	353	11	Q99N70	Q99n70 mus musculus
6	1336	31.1	732	6	Q9GLN6	Q9glN6 pan troglod
7	1329	31.0	1304	6	Q9GLN7	Q9glN7 pan troglod
8	1310	30.5	1313	11	Q9EQM9	Q9eqm9 rattus norv
9	1303	30.4	694	4	Q15540	Q15540 homo sapien
10	1089.5	25.4	648	5	Q9NDS8	Q9nds8 bombyx mori
11	1086	25.3	615	5	Q9NKE4	Q9nke4 drosophila
12	1057	24.6	660	5	Q17248	Q17248 boophilus m
13	1030	24.0	630	5	Q24222	Q24222 drosophila
14	1028	24.0	630	5	Q9VLJ6	Q9vlj6 drosophila
15	1004	23.4	249	11	Q9DB36	Q9db36 mus musculus
16	841	19.6	792	5	Q9VJV1	Q9vjv1 drosophila

17	642.5	15.0	907	5	Q18581	Q18581 caenorhabdi
18	502.5	11.7	661	5	Q9V520	Q9v520 drosophila
19	476	11.1	611	5	Q9VJV2	Q9vjv2 drosophila
20	434.5	10.1	202	11	Q64603	Q64603 rattus norv
21	409.5	9.5	628	5	Q9W021	Q9w021 drosophila
22	408.5	9.5	628	5	Q95U59	Q95u59 drosophila
23	390	9.1	222	11	Q9ESG3	Q9esg3 rattus norv
24	387	9.0	222	4	Q9HBJ8	Q9hbJ8 homo sapien
25	386	9.0	222	11	Q9ESG4	Q9esg4 mus musculu
26	306.5	7.1	121	6	Q9BDG1	Q9bdg1 bos taurus
27	280.5	6.5	135	4	Q16425	Q16425 homo sapien
28	251.5	5.9	157	11	Q61265	Q61265 mus musculu
29	239	5.6	75	5	Q9TX66	Q9tx66 drosophila
30	157	3.7	532	16	Q9KFV0	Q9kfV0 bacillus ha
31	152.5	3.6	734	5	Q9NKE3	Q9nke3 drosophila
32	147	3.4	54	6	Q95161	Q95161 canis fami
33	147	3.4	502	16	Q92AC3	Q92ac3 listeria in
34	139	3.2	608	16	Q9PR80	Q9pr80 ureaplasma
35	136	3.2	611	16	Q9PPW8	Q9ppw8 ureaplasma
36	130.5	3.0	461	2	Q9KI52	Q9ki52 enterococcu
37	127.5	3.0	3574	10	Q9AUB4	Q9aUb4 arabidopsis
38	127	3.0	779	5	Q9XYS8	Q9xys8 dictyostell
39	124.5	2.9	987	11	Q61636	Q61636 mus musculu
40	124.5	2.9	3429	11	O08614	O08614 mus musculu
41	124	2.9	53	6	O18865	O18865 canis fami
42	124	2.9	538	17	Q9YB20	Q9yb20 aeropyrum p
43	123.5	2.9	902	17	Q97Y10	Q97y10 sulfolobus
44	123.5	2.9	3419	11	O55147	O55147 rattus norv
45	123.5	2.9	5303	5	Q9V628	Q9v628 drosophila

ALIGNMENTS

RESULT 1

Q9NRA7 Q9NRA7 PRELIMINARY; PRT; 805 AA.
AC Q9NRA7:
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE ANGIOTENSIN CONVERTING ENZYME-LIKE PROTEIN (ACE-RELATED
DE CARBOXYPEPTIDASE ACE2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOMA;
RA Tiplis S.R., Hooper N.M., Hyde R.J., Christie G., Karran E.,
RA Turner A.J.;
RT "A Human Homolog of Angiotensin Converting Enzyme - Cloning and
RT Functional Expression As A Captopril-Insensitive Carboxypeptidase.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,
RA Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,
RA Breitbart R.E., Acton S.;
RT "A novel ACE-related carboxypeptidase (ACE2) converts angiotensin I to
RT angiotensin-1-9.";
RL Circ. Res. 0:0-0(2000).
DR EMBL; AF241254; AAF78220.1; -;
DR EMBL; AF291820; AAF99721.1; -;
DR MEROPS; M02.006; -;
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_MTpeptidse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIPTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Carboxypeptidase.

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SQ SEQUENCE 805 AA; 92462 MW; 8BE6E0A93155088 CRC64;
Query Match 100.0%; Score 4291; DB 4; Length 805;
Best Local Similarity 100.0%; Pred. No. 2e-305;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAGSTIEEQAKTFLDKFNHEAEDLFYQSSLSASWNTNTITEENVQ 60
DB 1 MSSSSWLLLSLVAVTAAGSTIEEQAKTFLDKFNHEAEDLFYQSSLSASWNTNTITEENVQ 60

QY 61 NNNAGDKWSAFLEKQSTLAQMYPLOEQNTLVKIQLOALQOQSSVLSDESKRLNTIL 120
DB 61 NNNAGDKWSAFLEKQSTLAQMYPLOEQNTLVKIQLOALQOQSSVLSDESKRLNTIL 120

QY 121 NTMSTIYSTGKVCNPDNPOECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
DB 121 NTMSTIYSTGKVCNPDNPOECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180

QY 181 EYVVLKNEMARANHYEDYDGYWRGDEYVNGVDGYDSRGOLIEDVHTFEIKPLYEHL 240
DB 181 EYVVLKNEMARANHYEDYDGYWRGDEYVNGVDGYDSRGOLIEDVHTFEIKPLYEHL 240

QY 241 HAYVRAKLMNAYPSYISPGICLPAHLGLDMGFRWNTLYSLTVPFGQKPNIDVTDAMVDQ 300
DB 241 HAYVRAKLMNAYPSYISPGICLPAHLGLDMGFRWNTLYSLTVPFGQKPNIDVTDAMVDQ 300

QY 301 AWDQRIKFEAEKFFSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRIILM 360
DB 301 AWDQRIKFEAEKFFSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRIILM 360

QY 361 CTKVYMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
DB 361 CTKVYMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420

QY 421 IGLLSPDFOEDNETEINFLLKQALITVGTLPFTYMLEKRWMMVFKEIPEKQKMMKKNWEM 480
DB 421 IGLLSPDFOEDNETEINFLLKQALITVGTLPFTYMLEKRWMMVFKEIPEKQKMMKKNWEM 480

QY 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYVYTRTLYQFOEQALCQAAKHEGPLH 540
DB 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYVYTRTLYQFOEQALCQAAKHEGPLH 540

QY 541 KCDISNSTAGOKLFNMLRLGKSEPTWLALENVVGAKNMVRLNLYFEPLFTWLKDQNK 600
DB 541 KCDISNSTAGOKLFNMLRLGKSEPTWLALENVVGAKNMVRLNLYFEPLFTWLKDQNK 600

QY 601 NSFGWSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMROYFLKVKY 660
DB 601 NSFGWSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMROYFLKVKY 660

QY 721 SLEFLGIQTLGPPNPQPPYSIHLIVGVVGMVIVGVITLITGTRDRKKKNKARSGENP 780
DB 721 SLEFLGIQTLGPPNPQPPYSIHLIVGVVGMVIVGVITLITGTRDRKKKNKARSGENP 780

QY 781 YASIDISKGNPNPGFQNTDDVQTSF 805
DB 781 YASIDISKGNPNPGFQNTDDVQTSF 805

RESULT 2
Q9BYF1 PRELIMINARY; PRT; 805 AA.
ID Q9BYF1
AC Q9BYF1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ACE2.
GN ACE2.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Komatsu T., Suzuki Y., Sugano S.; to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Suzuki Y., Watanabe M., Sugano S.;
RT "Cloning, expression analysis and chromosomal localization of a novel
RT ACE like enzyme."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046569; BAB40370.1; -.
DR InterPro; IPR001548; Peptidase_M2.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIPPTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 805 AA; 92491 MW; D2AAB4C27088EB72 CRC64;

Query Match 99.9%; Score 4288; DB 4; Length 805;
Best Local Similarity 99.9%; Pred. No. 3.4e-305;
Matches 804; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAGSTIEEQAKTFLDKFNHEAEDLFYQSSLSASWNTNTITEENVQ 60
DB 1 MSSSSWLLLSLVAVTAAGSTIEEQAKTFLDKFNHEAEDLFYQSSLSASWNTNTITEENVQ 60

QY 61 NNNAGDKWSAFLEKQSTLAQMYPLOEQNTLVKIQLOALQOQSSVLSDESKRLNTIL 120
DB 61 NNNAGDKWSAFLEKQSTLAQMYPLOEQNTLVKIQLOALQOQSSVLSDESKRLNTIL 120

QY 121 NTMSTIYSTGKVCNPDNPOECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
DB 121 NTMSTIYSTGKVCNPDNPOECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180

QY 181 EYVVLKNEMARANHYEDYDGYWRGDEYVNGVDGYDSRGOLIEDVHTFEIKPLYEHL 240
DB 181 EYVVLKNEMARANHYEDYDGYWRGDEYVNGVDGYDSRGOLIEDVHTFEIKPLYEHL 240

QY 241 HAYVRAKLMNAYPSYISPGICLPAHLGLDMGFRWNTLYSLTVPFGQKPNIDVTDAMVDQ 300
DB 241 HAYVRAKLMNAYPSYISPGICLPAHLGLDMGFRWNTLYSLTVPFGQKPNIDVTDAMVDQ 300

QY 301 AWDQRIKFEAEKFFSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRIILM 360
DB 301 AWDQRIKFEAEKFFSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRIILM 360

QY 361 CTKVYMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
DB 361 CTKVYMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420

QY 421 IGLLSPDFOEDNETEINFLLKQALITVGTLPFTYMLEKRWMMVFKEIPEKQKMMKKNWEM 480
DB 421 IGLLSPDFOEDNETEINFLLKQALITVGTLPFTYMLEKRWMMVFKEIPEKQKMMKKNWEM 480

QY 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYVYTRTLYQFOEQALCQAAKHEGPLH 540
DB 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYVYTRTLYQFOEQALCQAAKHEGPLH 540

QY 541 KCDISNSTAGOKLFNMLRLGKSEPTWLALENVVGAKNMVRLNLYFEPLFTWLKDQNK 600
DB 541 KCDISNSTAGOKLFNMLRLGKSEPTWLALENVVGAKNMVRLNLYFEPLFTWLKDQNK 600

QY 601 NSFGWSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMROYFLKVKY 660
DB 601 NSFGWSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMROYFLKVKY 660

QY 661 QMILFGEEDVRVANLKPRISNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDN 720
DB 661 QMILFGEEDVRVANLKPRISNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDN 720
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QY 721 SLEFLGIQPTLGGPPNPPVSIWLVGVVGMVIVGVIVILFTGIRDRKKKNKARSGENP 780
|||||
Db 721 SLEFLGIQPTLGGPPNPPVSIWLVGVVGMVIVGVIVILFTGIRDRKKKNKARSGENP 780
|||||
QY 781 YASIDISKGENNPGFQNTDDVQTSF 805
|||||
Db 781 YASIDISKGENNPGFQNTDDVQTSF 805
|||||

RESULT 3
Q9UFZ6 PRELIMINARY; PRT; 804 AA.
AC Q9UFZ6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 92.3 KDA PROTEIN (FRAGMENT).
GN DKFZP434A014.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL110224; CAB53682.1; -.
DR MEROPS; M02.006; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPTIDPTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 804 AA; 92340 MW; 91FF391074CB5DA9 CRC64;

Query Match 99.88; Score 4281; DB 4; Length 804;
Best Local Similarity 99.98; Pred. No. 1.1e-304;
Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSSSLLSLVAVTAAQSTIEQAKTFLDKFNHEADLFYQSSSLASWNYNTNITEENVQ 61
|||||
Db 1 SSSSLLSLVAVTAAHSTIEQAKTFLDKFNHEADLFYQSSSLASWNYNTNITEENVQ 60
|||||
QY 62 MNNAGDKWSAFLEKQSTLAQMYPLQEIQLTVKIQALQALQNGSSVLSDESKRLNTILN 121
|||||
Db 61 MNNAGDKWSAFLEKQSTLAQMYPLQEIQLTVKIQALQALQNGSSVLSDESKRLNTILN 120
|||||
QY 122 TMSYIYTGKVCNPDNPOECLELLPEGLNEINANSIDYNERLWAWESVRSEVGKQLRPLYE 181
|||||
Db 121 TMSYIYTGKVCNPDNPOECLELLPEGLNEINANSIDYNERLWAWESVRSEVGKQLRPLYE 180
|||||
QY 182 EYVVLKNEAMARNEYDGYDWRGDIYGVNGDYDYSRGQIEDVEHTFEIKRPLYEHLH 241
|||||
Db 181 EYVVLKNEAMARNEYDGYDWRGDIYGVNGDYDYSRGQIEDVEHTFEIKRPLYEHLH 240
|||||
QY 242 AYVRAKLNNAYPSYISPGCLPAHLGLDMGFRFTNLYSLTVPGQKPNIDVTAMDYDQA 301
|||||
Db 241 AYVRAKLNNAYPSYISPGCLPAHLGLDMGFRFTNLYSLTVPGQKPNIDVTAMDYDQA 300
|||||
QY 302 WDAQRIFEAKKFFVSVGLPNMTCGFENSMITDPGNVQKAVCHPTAWDLGKGFRLTLC 361
|||||
Db 301 WDAQRIFEAKKFFVSVGLPNMTCGFENSMITDPGNVQKAVCHPTAWDLGKGFRLTLC 360
|||||
QY 362 TKVTMDDFLTAHHEMGHIQYDMAAQQPFLIRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
|||||
Db 361 TKVTMDDFLTAHHEMGHIQYDMAAQQPFLIRNGANEGFHEAVGEIMSLSAATPKHLKSI 420
|||||
QY 422 GLLSPDFQEDNETEINFLKQALTIIVGLTPTYMLEKRWVVFKEIPKQDMKKKWKEMK 481
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Db 421 GLLSPDFQEDNETEINFLKQALTIIVGLTPTYMLEKRWVVFKEIPKQDMKKKWKEMK 480
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QY 482 REIVGVVEPVPHDETCDPASLFHVSNDYSFIRYTYTTLTYQFOFQALCOAAKEGELPHK 541
|||||
Db 481 REIVGVVEPVPHDETCDPASLFHVSNDYSFIRYTYTTLTYQFOFQALCOAAKEGELPHK 540
|||||
QY 542 CDSINSTEAGOKLPNMLRLGKSEPTWTLALENVGAKNNVRPLNLYPEPLFTWLKQDNKN 601
|||||
Db 541 CDSINSTEAGOKLPNMLRLGKSEPTWTLALENVGAKNNVRPLNLYPEPLFTWLKQDNKN 600
|||||
QY 602 SFVGMSTDMSPYADQSIKVRISLKSALGDKAYEWNDNEMVLFSSVAYAMROYFLKVKNO 661
|||||
Db 601 SFVGMSTDMSPYADQSIKVRISLKSALGDKAYEWNDNEMVLFSSVAYAMROYFLKVKNO 660
|||||
QY 662 MILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKEAIRMSRSRINDAFLRNDNS 721
|||||
Db 661 MILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKEAIRMSRSRINDAFLRNDNS 720
|||||
QY 722 LEFLGIQPTLGGPPNPPVSIWLVGVVGMVIVGVIVILFTGIRDRKKKNKARSGENP 781
|||||
Db 721 LEFLGIQPTLGGPPNPPVSIWLVGVVGMVIVGVIVILFTGIRDRKKKNKARSGENP 780
|||||
QY 782 ASIDISKGENNPGFQNTDDVQTSF 805
|||||
Db 781 ASIDISKGENNPGFQNTDDVQTSF 804
|||||

RESULT 4
Q99N71 PRELIMINARY; PRT; 798 AA.
AC Q99N71;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ANIGOTENSIN-CONVERTING ENZYME-RELATED CARBOXYPEPTIDASE.
GN ACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Yamada Y.,
RA Hida M., Tanigami A., Muroi S.;
RT Molecular cloning, mRNA expression, and chromosomal localization of
RT mouse Angiotensin-converting Enzyme-Related Carboxypeptidase.*;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB053181; BAB40431.1; -.
DR MEROPS; M02.006; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR000130; Zn_MTpeptdse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPTIDPTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Carboxypeptidase.
SQ SEQUENCE 798 AA; 91943 MW; 403AEA29D55725A4 CRC64;

Query Match 81.2%; Score 3485; DB 11; Length 798;
Best Local Similarity 82.2%; Pred. No. 1.9e-246;
Matches 644; Conservative 58; Mismatches 81; Indels 0; Gaps 0;

QY 1 MSSSSLLSLVAVTAAQSTIEQAKTFLDKFNHEADLFYQSSSLASWNYNTNITEENVQ 60
|||||
Db 1 MSSSSLLSLVAVTAAQSTIEQAKTFLDKFNHEADLFYQSSSLASWNYNTNITEENVQ 60
|||||
QY 61 MNNAGDKWSAFLEKQSTLAQMYPLQEIQLTVKIQALQALQNGSSVLSDESKRLNTILN 120
|||||
Db 61 MNNAGDKWSAFLEKQSTLAQMYPLQEIQLTVKIQALQALQNGSSVLSDESKRLNTILN 120
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QY 121 NTMTSTIYTGKVCNPDNPQECLELLLEPGLNETMANSLDYNERLWAWESVRSVGVKQLRPLY 180
Db 121 NTMTSTIYTGKVCNPKNPQECLELLLEPGLNETMANSLDYNSRLWAWEGVRAEVGKQLRPLY 180
QY 181 EBYVVLKEMARANEYEDYGDYWRGDIYEVNGVDGYDYSRGOLIEDVHTFEIKPLYEHL 240
Db 181 EBYVVLKEMARANNNDYGDYWRGDIYEAEGADGYNINRNQIIEVHTFAEIKPLYEHL 240
QY 241 HAYVRKLMDYPSYISPTGCLPAHLGDMGWFNTNLSYTVPPGKPNIDVTDAMVDQ 300
Db 241 HAYVRKLMDYPSYISPTGCLPAHLGDMGWFNTNLSYTVPPGKPNIDVTDAMNQ 300
QY 301 ANDAQRIKFAEKFFVSVGLPNMTQGWNSMLTDPGNVQKAVCHPTAWDLGKGFRLIM 360
Db 301 GWDARIFQAEKFFVSVGLPMTQGWNSMLTDPGNVQKAVCHPTAWDLGKGFRLIM 360
QY 361 CTYKVMDDFLTAHHEMGHIQYDMAYARQPFLLRNGANGSGFHEAVGEIMSLSAATPKHLKS 420
Db 361 CTYKVMDDFLTAHHEMGHIQYDMAYARQPFLLRNGANGSGFHEAVGEIMSLSAATPKHLKS 420
QY 421 IGLLSPDFOEDNTEINFLLKQALITVGTLPFTYMLEKRWMMVFKEIPKQWKKWEM 480
Db 421 IGLLSPDFOEDNTEINFLLKQALITVGTLPFTYMLEKRWMMVFKEIPKQWKKWEM 480
QY 481 KREIVGVVPEPHDETCDPASLFHVSNDYSFIRYTRTLTQFQAEALCOAAKHEGLH 540
Db 481 KREIVGVVPEPHDETCDPASLFHVSNDYSFIRYTRTLTQFQAEALCOAAKHEGLH 540
QY 541 KDISNSTAGOKLFLMLRGLKSEPTWLTALENVGAKNNVRPLINYPELFTWLKDQNK 600
Db 541 KDISNSTAGOKLFLMLRGLKSEPTWLTALENVGAKNNVRPLINYPELFTWLKDQNK 600
QY 601 NSFVGVSTDSYADQSIKVRISLSKALGDKAYENDNEMYLFRSSVAYAMRQYFLKYK 660
Db 601 NSFVGVSTDSYADQSIKVRISLSKALGDKAYENDNEMYLFRSSVAYAMRQYFLKYK 660
QY 661 QMLFGSEDRVANLKPRTISFFFTVAPKNVSDIIPRTVEVKAIRMSRSRINDAFLRNDN 720
Db 661 QVTFLEDRVRSDLKPRYSFFFTVAPKNVSDIIPRTVEVKAIRMSRSRINDAFLRNDN 720
QY 721 SLEFLGIOTPLGPPNPPVSWLVGVVGVVGVIVLIFTGRDRKKKNAKRSNGP 780
Db 721 SLEFLGIOTPLGPPNPPVSWLVGVVGVVGVIVLIFTGRDRKKKNAKRSNGP 780
QY 781 YAS 783
Db 781 YDS 783

RESULT 5
Q99N70 PRELIMINARY; PRT; 353 AA.
AC Q99N70;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ANIGOTENSIN-CONVERTING ENZYME-RELATED CARBOXYPEPTIDASE.
GN ACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Ymada Y.,
RA Hida M., Tanigami A., Muroi S.;
RT "Molecular cloning, mRNA expression, and chromosomal localization of
RT mouse Angiotensin-converting Enzyme-Related Carboxypeptidase.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Suzuki Y., Hanaoka K., Yamada Y.;
RT "Molecular cloning of ACE2.";
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RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB053182; BAB40432.1; -.
DR MEROPS; M02.006; -.
DR InterPro; IPR001548; Peptidase_M2.
DR Pfam; PF01401; Peptidase_M2; WD40.
DR PRINTS; PR00791; PEPTIDTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Carboxypeptidase.
SQ SEQUENCE 353 AA; 40442 MW; D17B71141EE4AF5B CRC64;

Query Match 35.9%; Score 1539; DB 11; Length 353;
Best Local Similarity 81.2%; Pred. NO. 1.5e-104;
Matches 285; Conservative 22; Mismatches 44; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAQAOSTIEQAKTFLEKFNHEARDLFYQSSLASWNTNTITEENVQ 60
Db 1 MSSSSWLLLSLVAVTTAQSILTEENAKTFLENFQAEADLSYQSSLASWNTNTITEENAQ 60
QY 61 MNMAGDKWAFLEKEQSTLAQMYPLQBIQNTVKLOLQALQOQSSSVLSKSKRLNTIL 120
Db 61 KMSEAAKWSAFVEQSKTAQSFSLQEIQTPIIKRQLQALQOQSSSALSADKNKQLNTIL 120
QY 121 NTMTSTIYTGKVCNPDNPQECLELLLEPGLNETMANSLDYNERLWAWESVRSVGVKQLRPLY 180
Db 121 NTMTSTIYTGKVCNPKNPQECLELLLEPGLNETMANSLDYNSRLWAWESVRSVGVKQLRPLY 180
QY 181 EBYVVLKEMARANEYEDYGDYWRGDIYEVNGVDGYDYSRGOLIEDVHTFEIKPLYEHL 240
Db 181 EBYVVLKEMARANNNDYGDYWRGDIYEAEGADGYNINRNQIIEVHTFAEIKPLYEHL 240
QY 241 HAYVRKLMDYPSYISPTGCLPAHLGDMGWFNTNLSYTVPPGKPNIDVTDAMVDQ 300
Db 241 HAYVRKLMDYPSYISPTGCLPAHLGDMGWFNTNLSYTVPPGKPNIDVTDAMNQ 300
QY 301 ANDAQRIKFAEKFFVSVGLPNMTQGWNSMLTDPGNVQKAVCHPTAWDL 351
Db 301 GWDARIFQAEKFFVSVGLPMTQGWNSMLTDPGNVQKAVCHPTAWDL 351

RESULT 6
Q99N70 PRELIMINARY; PRT; 732 AA.
AC Q99N70;
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DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE DIPEPTIDYL CARBOXY PEPTIDASE 1 TESTICULAR FORM.
GN DCF1.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20469400; PubMed-11013071;
RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
RA Jeunenaitre X.;
RT "Human-Chimpanzee DNA sequence variation in the four major genes of
RT the renin angiotensin system.";
RL Genomics 69:14-26(2000).
DR EMBL; AF193486; AAG31359.1; -.
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DR PRINTS; PR00791; PEPTIDTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 732 AA; 83428 MW; C43D06443A47E74B CRC64;

Query Match      31.1%; Score 1336; DB 6; Length 732;
Best Local Similarity 41.6%; Pred. No. 3.2e-89;
Matches 258; Conservative 119; Mismatches 205; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKTFIDKFHAEADLFYQSSLASNNYNTNITEE-----NVQNM 62
DB 61 TSAQSPNLVTDAAEASKFVEEDRTSQVVNVEYAEANNYNNTNITTSKILLQKNMQIA 120
QY 63 NNAGDKWSAFLKEQSTLAQMYPLQETQNLTKVQLQALQOQNGSSVLSSEKSKRLNTILNT 122
DB 121 NHT-----LKYGCTQARRFDVNLQNTTKRIKKVQDILERALPAQELLEYNKILLD 172
QY 123 MNTIYSTGKVPNDPQCLLEPGCLNEIMANSLDYNRLWAWESWRSEVGKQLRPLYEE 182
DB 173 METTYSVATVCHTNG--SCLQLEPDLTNVMATSRKYEDLLWAWGWRDKAGRAILQFPYK 230
QY 183 YVVLAKENARANHVEDYGDYWRGDEVGVNGDYDYSRQLTIEDVHTFEELKPLYEHLHA 242
DB 231 YVELINQARLINGYDAGDSWRSMTETPSLE-----QDLERLQFQELPYLYNLHA 280
QY 243 YVRAKLMNAY-PSYISPGCLPAHLGDMGFRFTNLSLVFPQCQPNIDVTDAMVDQA 301
DB 281 YVRRALHRHYGAQHINLEGPPIPAHLGNWQAQTSNIYDLVVPFAPSMDTTEAMLKQG 340
QY 302 WDAQRIKFAEAEFFVSGLPNWTOGFWENSMLTDPGNVOKAVCHPTAWDLGKG--DFRILM 360
DB 341 WTPRRKFEADDFTSGLLPPVPEFWNKSMLERKPTDGREVVCHASAWDFYNGKDFRIK 400
QY 361 CTKVTMDDFLAHHEMGHIQYDMAAQAQPFLLRNGANGPHEAVGEIMSLSAATPKHLKS 420
DB 401 CTTVNLDELVAHHEMGHIQYFMQYKDLPLVALREGANPGFHEALGDVLALSVPKHLHS 460
QY 421 IGLLSPDQDENEINFLKQALITVGTLPFTYMLEKRWMMVFKGIPKQDMKKWEM 480
DB 461 LNLISSEGGSD-EHDINFLMKALDKIAFIPSYLVQDWRWRVFGSGITKENYNQEWWSL 519
QY 481 KREITGVVPEVPHDETCDPASLFHVSNDYSFIRYRTLTLYQFOFQALCOAAKHEGPLH 540
DB 520 RLKVGGLGCPVPRQTGGDFDGAKEHIPSSVPYIRYFVSFIQFQFHEALCOAAGHTGLH 579
QY 541 KCDISNSTEAGQKLFNMLRLGKSPWTLALENVYGAKNMVRPLLNYFEPLFTWLKQDNK 600
DB 580 KCDIYQSEAGQRLATAMKLGFSRPWPEAMGLIINGQPNMSASAMLSFTKPLLDWLRTENE 639
QY 601 --NSFVGW-STDNWSPYADQS 617
DB 640 LHGEKLGWPOYNWTPNSARS 659

RESULT 7
Q9GLN7 PRELIMINARY; PRT; 1304 AA.
AC Q9GLN7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DIPEPTIDYL CARBOXY PEPTIDASE 1.
GN DCPI.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
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RP SEQUENCE FROM N.A.
RX MEDLINE=20469400; PubMed=11013071;
RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
RA Jeunenaitre X.;
RT "Human-Chimpanzee DNA sequence variation in the four major genes of
RL the renin-angiotensin system.";
RL Genomics 69:14-26(2000).
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DR EMBL; AF193829; AAG31358.1; JOINED.
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DR EMBL; AF193848; AAG31358.1; JOINED.
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DR EMBL; AF193850; AAG31358.1; JOINED.
DR EMBL; AF193851; AAG31358.1; JOINED.
DR EMBL; AF193852; AAG31358.1; JOINED.
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DR EMBL; AF193854; AAG31358.1; JOINED.
DR EMBL; AF193855; AAG31358.1; JOINED.
DR EMBL; AF193856; AAG31358.1; JOINED.
DR EMBL; AF193857; AAG31358.1; JOINED.
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DR EMBL; AF193863; AAG31358.1; JOINED.
DR EMBL; AF193864; AAG31358.1; JOINED.
DR EMBL; AF193865; AAG31358.1; JOINED.
DR EMBL; AF193866; AAG31358.1; JOINED.
DR EMBL; AF193867; AAG31358.1; JOINED.
DR EMBL; AF193868; AAG31358.1; JOINED.
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DR EMBL; AF193872; AAG31358.1; JOINED.
DR EMBL; AF193873; AAG31358.1; JOINED.
DR EMBL; AF193874; AAG31358.1; JOINED.
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Db 982 VVAHEMHGHIQFYMQYKDLPLVALREGANPGFHEAIGDVLALSVPKPHLSHLLSSEGG 1041
Qy 430 EDNETEINFLKQALITVGTLPFTYMLEKRWVYFKEIPKQDQWKKWEMKREIVGVVE 489
Db 1042 SD-EHDINFLMKALDKIAFIPFSYLDQWRWRVFDGSIYKENTQWNSLRUKYQGLCP 1100
Qy 490 PVPDHTVCDPASFHNSDYSFIRYTRTYLQFQFQALCOAAKHGGLHKKDCISNSTE 549
Db 1101 PVPQTGDFDCAKHFHPSSVPYIRYFVSFIQFQFHEALCOAAGHTGPLHKDCIYQSK 1160
Qy 550 AQOKLFNMLRGKSEPTWLTALENVVGAKNMVRPLLYFPELFTWLKDQNK--NSFVGV- 606
Db 1161 AGORLATAMKLGFSRPWPEAMQLITGPNMSASAMLSYFKPLDPLDLRTENELHGEKLG 1220
Qy 607 STDSPYADQS 617
Db 1221 QYNWTPNSARS 1231

RESULT 8
Q9EQM9 PRELIMINARY; PRT; 1313 AA.
ID Q9EQM9
AC Q9EQM9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANGIOTENSIN-CONVERTING ENZYME.
GN ACE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F344/N; TISSUE=LUNG;
RA Jafarjan-Tehrani M., Listwak S., Barrientos R.M., Michaud A.,
RA Corvol P., Sternberg E.M.;
RT *Characterization of a missense mutation in the angiotensin I-
RT converting enzyme cDNA in exudative inflammation resistant F344/N
RT rats.*
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201331; AAC35596.1; -.
DR InterPro; IPR001109; HupF_Hypc.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_Mtpeptidse.
DR Pfam; PF01401; Peptidase_M2; 2.
DR PRINTS; PR00791; PEPTIDTASEA.
DR ProDom; PD004184; Peptidase_M2; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 1313 AA; 150941 MW; E888341562542B04 CRC64;

Query Match 30.5%; Score 1310; DB 11; Length 1313;
Best Local Similarity 42.0%; Pred. No. 5.9e-87;
Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;

Qy 20 TIEQAKTFLDKFHEADLFYQSSLASWYNTNTTEENVQNMNAGDKWSAFLEKQSTL 79
Db 650 TDEAKANREVEEDRTAKVILNEYAEANWHYNTNITIEGSKILLQKNKREVSNHTLYGTW 709
Qy 80 AQMPLOETQNTLVKLOALQONGSSVLSDEKSKRLNTILMTSTIYTGKVCNPDNPQ 139
Db 710 AKTFVDSNFQNSTIKRIKKNQVDRVLPPELEYYNOILDMETTYSVANVCYTG-- 767
Qy 140 ECILLFPGLNEIMANSLDYNERLAWESWRSEVGKQLRPLYEYVVLKNEMARANHYEDY 199
Db 768 TCLSLEPDLTNIMATSKRYEELLWYKSWRDKVGRALLPFPKPYVDFSNKIAKLGYSDA 827
Qy 200 GYWRGDYEVNGVDGYDSRGQIEDVEHTFEIKPLYLEHLHAYVRKLMNAYS-YISP 258
Db 828 GDSWRSSYESDDLE-----QDLEKLYQELQPLYLNLHAYVRRALHRRHYGSEYINL 877
Qy 259 IGLPRLHGLDMWGRFTWNLVSLTVFPGOKPNIDVTDMVDQAWDAQRIKFAEKFVSV 318
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Db 878 DGPFAHLHGNMAQWTSNIYDLVAPFPSPASIDATEAMIKQGTWPRRIFKEADNFTSL 937
Qy 319 GLPNMTQGFENSMITDPGNQVQKAVCHPTAWDLGK--DFRILMCKTXYTMDDFLTAHEMG 377
Db 938 GLLPVPPEFWNKSLEKPTDGRVNVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHEMG 997
Qy 378 HIQYDMAYAAQFLLRNGANEGFHEAVGIMSLSAATPKHLKASIGLLSPDFQEDNETEIN 437
Db 998 HIQYFQYKDLPLVTFREGANPGFHEAIGDVLALSVPKPHLSHLLSSE--GSGYEHDIN 1056
Qy 438 FLKQALITVGTLPFTYMLEKRWVYFKEIPKQDQWKKWEMKREIVGVVPEPHDITY 497
Db 1057 FLMKALDKIAFIPFSYLDQWRWRVFDGSIYKENTQWNSLRUKYQGLCPVPRSQGD 1116
Qy 498 CDPASLFHNSDYSFIRYTRTYLQFQFQALCOAAKHGGLHKKDCISNSTEAGOKLFNM 557
Db 1117 FDPGSFHPVNPYIRYFVSFIQFQFHEALCRAAGHTGPLYKDCIYQSKAGKLLADA 1176
Qy 558 LRLGKSEPTWLTALENVVGAKNMVRPLLYFPELFTWLKDQNK--NSFVGV-STDHSP 612
Db 1177 MKLGSKQWPEAMKIITGPNMSASAIMNYFKPLTEMLVTENRRHGETIGWPEYTWTP 1234

RESULT 9
Q15540 PRELIMINARY; PRT; 694 AA.
ID Q15540
AC Q15540;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DCP1 PROTEIN.
GN DCP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90046671; PubMed=2554286;
RA Ehlers M.R., Fox E.A., Strydom D.J., Riordan J.F.;
RT *Molecular cloning of human testicular angiotensin-converting enzyme:
RT the testis isozyme is identical to the C-terminal half of endothelial
RT angiotensin-converting enzyme.*
RL Proc. Natl. Acad. Sci. U.S.A. 86:7741-7745(1989).
DR EMBL; M26658; AAA60612.1; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_Mtpeptidse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPTIDTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 694 AA; 79333 MW; 57C0FF9C5AEC119 CRC64;

Query Match 30.4%; Score 1303; DB 4; Length 694;
Best Local Similarity 42.7%; Pred. No. 7.7e-87;
Matches 250; Conservative 107; Mismatches 195; Indels 34; Gaps 9;

Qy 45 LASWYNTNITEE-----NVQNMNAGDKWSAFLEKQSTLAQMYPLQEIQNLTVKLO 96
Db 57 IATKNYNTNITETSKILLQKNMQIAHNT-----LKYGTQARKFDVHQLQNTTIKRI 108
Qy 97 LOALQONGSSVLSDEKSKRLNTILMTSTIYTGKVCNPDNPQRCLELLEPLNEIMANSL 156
Db 109 IKKVQDLERAAALPAQEEYKNILLDMETTYSVATVCHPNQ--SCLQLEPDLTNVMAISR 166
Qy 157 DYNERLAWESWRSEVGKQLRPLYEYVVLKNEMARANHYEDYGYWRGDYEVNGVDGYD 216
Db 167 KYEDLLAWEGWRDKAGRAILLQFYPKYVELINQAARLNGYVDAGDSWRSMYETPSLE--- 223
Qy 217 YSRGQIEDVEHTFEIKPLYLEHLHAYVRKLMNAY-PSYISPIGCLPAHLHGLDMWGRF 275
Db 224 -----QDLERLQELQPLYLNLHAYVRRALHRRHYGAQHINLEGPIPAHLHGNMAQW 276
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QY 276 TNLVSLTVFGQKPNIDVTDAVDQADQIRFKEAEKFFVSVGLPNMTQGFWNSMLTD 335
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 277 SNIDLVVFPSPAPSMTTEMLKQGWTPRMFKFADDEFTSLGLLPVPPFENKSMLEK 336
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 336 PGNVQKAVCHPTAWDLGKG-DPRILMCTKVTWDDFLTAHHMGHTIOYDMAYAAQFFLLRN 394
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 337 PYDGGREVVCHASAWDFYNGKDFRIKQCTTVNLEDJVAHHMGHTIOYFQYKDLPLVALRE 396
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 395 GANEGFHEAVGIMSLSAATPKHLKSLGLSPDFOEDNETEINFLKQALITVGTLPETY 454
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 397 GANPGFHEAIGDVLALSVPKHLHSLNLLSEGGSD-EHDINFLMKWALDKIAFIPPSY 455
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 455 MLEKRWVVFGEIPKQDMKKWPMKREIVGVVPEVPHDETYCDPASLFVNSNDYSIR 514
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 456 LVDQNRWRVFDGSIKTENYNGWMSLRKYGCLCPVPRTQGDPPGAKFIHPSSVPYIR 515
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 515 YVTRLYQFOQEALCOAKHEGPHLKCDISNSTEAGOKLFNMLRLGKSEPTWLTALENVV 574
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 516 YFVSFIIOQFHEALCOAGHTGPHLKCDIYQSKAEGORLATAMKLGFSRPWPEAMOLIT 575
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 575 GAKNNVRPLNRYEPFLTWLKDQNK--NSFVGW-STDWSVYADQS 617
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 576 GQPNMSASAMLSYRKPILLDRLTENELHGEKLGHPQYNWTPNSARS 621
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 10
Q9NDS8
ID Q9NDS8 PRELIMINARY; PRT; 648 AA.
AC Q9NDS8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ECYSTEROID-INDUCIBLE ANGIOTENSIN-CONVERTING ENZYME-RELATED GENE
DE PRODUCT.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C108; TISSUE=WING IMAGINAL DISK;
RX MEDLINE=20556050; PubMed=11102839;
RA Qian G.X., Mita K., Okano K., Shimada T., Ugalin N., Xia Z., Goto N.,
RA Kanke E., Kawasaki H.;
RT *Isolation and expression of the ecysteroid-inducible angiotensin-
RT converting enzyme-related gene in wing discs of Bombyx mori.*;
RL Insect Biochem. Mol. Biol. 31:97-103(2001).
DR EMBL; AB026110; BAA97657.1; -.
DR MEROPS; M02.002; -.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_MTpeptidse.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDPTASEA.
DR ProDom; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 648 AA; 74917 MW; 9A740AA9FCACEBF0 CRC64;

Query Match 25.48; Score 1089.5; DB 5; Length 648;
Best Local Similarity 35.68; Pred. No. 2.9e-71;
Matches 23; Conservative 125; Mismatches 259; Indels 35; Gaps 11;

QY 11 LVAYTAAQSTIEEQAQ-TFLDKFNHEAEDLFY-----QSSLASNYNTNITEEN 58
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 59 VQNNNAGDKWAFLEKQSTLAQMPLEQTONTUTVKLQALQOQSSVLSDESKRLNT 118
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 70 EKSIOETHLSROEKAWEETKMYGQWQDFQDFTLRMKKYSQGLVAALPDDKQALMR 129
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 119 ILNTMSTIYSTGKVCNPDNPOEC-LLEPLGELNEIMANSLDYNRELNAWESWRSEVQKLR 177
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 130 TVSGHESNYATAKICSYKNKSCDLSLEPEITTEIFTSQDPPEELKHAWEVHNAAGATAK 189

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QY 178 PLYEYVVLKNEMARAHYEDYDWRGDEYVNCVQDYDYSRGQLIEDVHTFEEIKPLY 237
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 190 KNFTDYVNLNEAAKLAGFDNVAEWQSEYEPDPE-----BQLAKLWEDVKPLY 239
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 238 EHLHAYVRKILMAY-PSYISPIGLPAHLGDMGWFNLTSLVDFGOKPNIDVTDA 296
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 240 QQLHAYVRKRLRDYKGDVVSARGPIFAHLGLGNMAQTWNIESFTPRYFDKKEIDVTQA 299
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 297 MVDQANDQARIFKEAEKFFVSVGLPNMTQGFWNSMLTDGCVQKAVCHPTAWDLGKG-D 355
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 300 MRDQNYTPMKMFQMSDEFFRSLNLTAMPEKFWKNSIIEKPTD-REIVCHASAMWDFDGED 358
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 356 FRILMCTKVTWDDFLTAHHMGHTIOYDMAYAAQFFLLRNGANGEGFHEAVGIMSLSAATP 415
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 359 FRIKOCYTVDEYFQTTHEMHGHTIOYLRDQPVFVRDGANQGFHEAVGDTIALSVSSP 418
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 416 KHLKISGLSPDFOEDNETEINFLKQALITVGTLPETYMLEKRWVVFGEIPKQDMKK 475
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 419 KHLRRVGLATGD-AEDQTEINQLYKMGIDKIAFLPAYTLDLFRYGVFRKRLPYEDYNC 477
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 476 KWMEMKREIVGVVPEVPHDETYCDPASLFVNSNDYSIRYTRTYLQFOQEALCO-AAK 534
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 478 HYWKLEQLOGVEPPVNRTEDEDDFAAKYHVSSNVEYARYVSVFIQFPHRGVCQLAGE 537
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 535 HEG-----PLHKCDISNSTEAGOKLFNMLRLGKSEPTWLTALENVVGNKNNVRPLNRYFE 589
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 538 HAAGDPNKKLVDCDIYQSVAAAGNALANMLKMGSKKMPDAMEALTQOREKADGLLEYFR 597
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 590 PLETLWKDQNKNS--FVGWSTDWSVYADQSIKVRISLKSALGDKAVENDN 638
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 598 PLHDWLRAENQRTGEHIGWEPNTNWEYCTPSQLSELNVKFESSSPATQSDS 648
Db :||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 11
Q9NKE4
ID Q9NKE4 PRELIMINARY; PRT; 615 AA.
AC Q9NKE4; Q9VJ3V3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANCE PROTEIN (LD11258P).
GN ANCE OR BG:DS08220.3 OR CG8827.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Phyllophaga; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Rote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Gelniker S., Rubin G.M.;
RA "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RA Gelniker S.E., Agbayani A., Arcalca T.T., Baxter E., Blazej R.G.,
RA Butenhoif C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Swirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]

```

RP	SEQUENCE FROM N.A.	
RC	STRAIN-BERKELEY;	
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,	
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,	
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,	
RA	Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,	
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	
RA	Borkova D., Botchan M.R., Bouck J.J., Brokstein P., Brotter P.,	
RA	Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RA	Dodson K., Doup L.E., Downes M., Duran Rocha S., Dunkov B.C., Dunn P.,	
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RA	Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,	
RA	Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,	
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,	
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	
RT	"The genome sequence of <i>Drosophila melanogaster</i> ."	
RL	Science 287:2185-2195(2000).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-Y, CN BW SP;	
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,	
RA	Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,	
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,	
RA	Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,	
RA	Yu C., Lewis S.E., Rubin G.M., Celniker S.;	
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AE003408; AAF44834.1; -	
DR	EMBL; AE003641; AAF53353.2; -	
DR	EMBL; AV061129; AAL28677.1; -	
DR	FlyBase; FBgn012037; Ance	
DR	InterPro; IPR001548; Peptidase_M2.	
DR	InterPro; IPR000130; Zn.Mrpeptdse.	
DR	PRINTS; PR00791; PEPTIDPTASEA.	
DR	PRODOM; PD004184; Peptidase_M2; 1.	
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.	
SQ	SEQUENCE 615 AA; 70913 MW; 9E3691BCC51D6C48 CRC64;	
Query Match	25.3%; Score 1086; DB 5; Length 615;	
Best Local Similarity	36.4%; Pred. NO. 4.9e-71;	
Matches 223; Conservative 122; Mismatches 245; Indels 22; Gaps 9;		
QY	8 LLSLVAVTAQSTIEEQAKTFLDKFNHEADLFYQSSLASWNYNTNTEENVQNNAGD 67	
DB	8 LLATLATVQALVKKEIQAKLENIENKELAKRTNVTETAAYGNSITDENKKKEISA 67	
QY	68 KWSAFLEKQSTLAQMPLQEQNLTKVLQALQONGSSVLSEDSKRLNTINTWSTIY 127	
DB	68 ELAKFNKEVASDTTKFQWRSYQSEDLKRFQKALTALIGYAALPEDDYAELDLTSLASNSF 127	
QY	128 STGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAMESRSEVSGKOLRDLPEYVVL 186	
DB	128 AKVVCYDKNDSTKCDLALDPEIEVLKSRDHEELAYYWRFEYDKAGTASQOFERYVEL 187	
QY	187 KNEMARANHEDYGDYWRGDYEVNGVDYDYSRGQLIEDVEHTEFEIKPLYEHLHAYVRA 246	
DB	188 NTKAAKLNNFTSGAEAWLDEYE-----DDTFEQOLEDI---FADIRPLYQIHGYVRF 237	
QY	247 KLMNAY-PSYISIPGCLPAHLGLGDMGFWNTNLSYLPFGQKPNIDVDTDAMVDQAWDAO 305	
DB	238 RLKHYGDVAVSETGPIPHILLGNMAQKQSEIADIVSPFPEKPLVDVSAEMEKQGYTPL 297	
QY	306 RIFKEAEKFPVSVGLNMTQGFWENSMITDPCGNQKAVCHPTAWDLG-KGDFRILMCTKV 364	
DB	298 KMFQMGDDFTSNLTKLFQDFWKSIIIEKPTDGRDLVCHASAWDFYLTDDVRKQCTKV 357	
QY	365 TMDEFTAHHEMGHIOYDMAYAAOPFLLRNAGNEGHEAVGEIMSLSAATPHLKSIGLL 424	
DB	358 TQDLFTVHHELGHITFYQYQHPFVYRTGANGPGEAVGDLVLSVSTPKHLEKIGLL 417	
QY	425 SPDFQEDNETEINFLKQALTIYGTLPFTYMLEKWRMVPKGEIPKQDWMKWKWEMKREI 484	
DB	418 K-DYVRDDEARINQLFTALDKIVFLPFAFTMDKYRWSLFRGEVDKANWNCFAWKLDEY 476	
QY	485 VGVPEVPVPHDETCDPASLHVNSDYSFIRYTYTLYQFQFQALC-QAAKH-----EGP 538	
DB	477 SGIEPPVVRSEKDFDAPAKYHISADVEILYLSVFIQFQFYKSACIKAGQYDDNPVLP 536	
QY	539 LHKCDISNSTEAGKLFNMLRLGKSPFTLALENVYGAKNMNVRLNLYPEPLFTWLKQD 598	
DB	537 LNCNDIYSSAAGAAAFHNMLSMGAKFPDPALEAFNGERIMSGKATAEYFELRVWLEAE 596	
QY	599 N--KNSFEVGMST 608	
DB	597 NIKNNVHIGWTT 608	
RESULT 12		
Q17248	PRELIMINARY; PRT; 660 AA.	
ID	Q17248	
AC	Q17248;	
DT	01-NOV-1996 (TrEMBLrel. 01, Created)	
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	ANGIOTENSIN-CONVERTING ENZYME-LIKE PROTEIN PRECURSOR.	
GN	BM91.	
OS	Boophilus microplus (Cattle tick).	
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;	
OC	Parasitiformes; Ixodida; Ixodidae; Boophilus.	
OX	NCBI_TaxID=6941;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Whitfield P.L., Johnson M.C., Smith D.R.J., Shelson V.J., Clifton G.F.,	
RA	Brown G.S., Cairns D., Foy A.B., Irving D.O.;	
RT	"The Cloning of an Angiotensin-Converting Enzyme cDNA from the Cattle	
RT	Tick <i>Boophilus microplus</i> ."	
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; U62809; AAB04998.1; -	
DR	MEROPS; M02.0PW; -	
DR	InterPro; IPR001548; Peptidase_M2.	
DR	Pfam; PF01401; Peptidase_M2; 1.	
DR	PRINTS; PR00791; PEPTIDPTASEA.	
DR	PRODOM; PD004184; Peptidase_M2; 1.	
KW	SIGNAL.	
FT	SIGNAL 1 29 POTENTIAL.	
FT	CHAIN 30 660 POTENTIAL.	
SQ	SEQUENCE 660 AA; 75257 MW; 6F164CF70C938B63 CRC64;	
Query Match	24.6%; Score 1057; DB 5; Length 660;	
Best Local Similarity	37.2%; Pred. No. 7.2e-69;	
Matches 226; Conservative 110; Mismatches 237; Indels 34; Gaps 13;		
QY	11 LVAVTAQSTIEEQAK--TFLDKFNHEADLFYQSSLASWNYNTNTEENVQNNMN-AGD 67	

Db	36	L	ATLSNVSAKLDKDEAMGVAFIEGLNDPYYTINNVDSSSSWDYASNTIDYN-QNMSKNVST	94
Qy	68	K	WSAFLEKQSTIAOYPLQEIQNITVKLOLQALQQNGSSVLSDEGSKRLNTILNTASTIY	127
Db	95	E	VSKMERQFGITAKRFDFWHNFKNDSLKRLFRHVATIGLAALPDDKLENATSLSSKMAAY	154
Qy	128	S	TGKVC---NPDNPQECLLLEPGLNETIWMNSLDYNERLAWESWRSEVQKQLRPLYEYV	184
Db	155	G	STKVTYGVKKDLP-----LEPDTRNNKEVGYDKILOTLWLAWHNAVGPATKQYYIPYI	209
Qy	185	V	LKKNEMARAHYEDYDGYWRGDYEVNGVDYDSRGOLIEDVHTFEETKPIYEHHLHAV	244
Db	210	K	LSNEAASLDGYDNIKSAWLSDYETE-----NMTEIVDKLWEDLSPLYKKLHAVY	259
Qy	245	R	AKLNNAYPYSIIPIGCLPAHLGLDMMGRFTWNLV-SLVVPFGQKPNIDVTDAMVDQAND	303
Db	260	R	KRIREIYPGRLPDGTPPAHLGLGNMAQEWGTLYPHLTME---DKP-LOISKTWVBQKWD	316
Qy	304	A	QRIFFKEAEKFFVSVGVPNNMTQGFWNSMLTDPGNQKAVCHPMTADMLCKG-DFRILMCT	362
Db	317	A	QKMFHAEDFFTSGLDNTSEFWSKIUTKEPD-RETOCHASAWNMTNGDFFRIKMTCT	375
Qy	363	K	VTMDDELTAHHMGHTQYDMAYAAQOFLRLRNGANEGFHEAVGEIMSLSAATPKHLKSGI	422
Db	376	D	PSVEELTRVHHMGHIEYYMQYKHLVLLOQEGANEGFHEAVGDLIALSVATKTHYGKLS	435
Qy	423	L	LSPDFQEDNETEIFLLKALITVGTLPPTYMLEKRWVFKGEIPKQWKKKWEKWR	482
Db	436	L	LKP---TDKYNADVLLMSALOKIAFLPPGYLLDKRWTFITGETFPDKMKEKFWEYRI	492
Qy	483	E	IVGVFVPHDETYCDPASLFSVNDYISFIRYTTLTLYQFQFQALCOAAK---HEGPL	539
Db	493	K	YQGVSPVPVRNSESFDGGAKYHVALHVPLYRVFVAFILQFQFHEHLCITVAKKVDHEHPF	552
Qy	540	H	KCDISNSTEAGQKLFNMLPLGKSEFWTALENNVGAKMNVVRPLUNYEEPLFTWLKQDN	599
Db	553	H	ECDIYGEKNAGDVLKGLSLGRSKPMPDYLEIMAGTROMSASSLKKYYEPLKWLDERI	612
Qy	600	K	NSFVGV	606
Db	613	K	NEVGVG	619

RESULT 13	
Q24222	PRELIMINARY; PRT; 630 AA.
ID	Q24222;
AC	Q24222;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	METALLOPEPTIDASE (ANGIOTENSIN-CONVERTING ENZYME-RELATED PROTEIN).
GN	ACER OR CG10593.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID:7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE-97128790; PubMed-8973330;
RA	Taylor C.A.M., Coates D., Shirras A.D.;
RT	"The Acer gene of Drosophila codes for an angiotensin-converting
RT	enzyme homologue.;"
RL	Gene 181:191-197(1996).
	[2]
RP	SEQUENCE FROM N.A.
RP	STRAIN-BERKELEY;
RC	Celniker S.E., George R.A., Galle R., Swirskas R.R., Hoskins R.A.,
RA	Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Chavez C., Chew M.,
RA	Doyle C.M., Farfan D.E., Flanagan J., Houston K.A., Hummasti S.R.,
RA	Karra K., Kearney L., Kim S.H., Lee B., Lomotan M.A., Mak J.,
RA	Mazda P., Mok M.S., Moshrefi A.R., Moshrefi J.M., Nixon K. Pacleab J.M.,

RA	Park S., Pfeiffer B., Punch E., Snir E., Twomey B., Wan K.H.,
RA	Whitelaw K.R., Yee A., Zhang R., Zieran L.L., Kimmel B.E.,
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; X96913; CAA65632.1; -
DR	EMBL; AC004728; -; NOT_ANNOTATED_CDS.
DR	Flybase; FBgn0016122; Acer.
DR	InterPro; IPR001548; Peptidease_M2.
DR	pfam; PF01401; Peptidease_M2; 1.
DR	PRINTS; PR00791; PEPTIDTASEA.
DR	PRODOM; PD004184; Peptidease_M2; 1.
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT	CONFLICT 236 L -> F (IN REF. 2).
FT	CONFLICT 341 Q -> H (IN REF. 2).
FT	CONFLICT 528 V -> A (IN REF. 2).
SQ	SEQUENCE 630 AA; 73042 MW; 248kAB90319BC32D CRC64;

Query Match	24.0%; Score 1030; DB 5; Length 630;
Best Local Similarity	35.6%; Pred. No. 6.3e-67;
Matches 219; Conservative 113; Mismatches 260; Indels 24; Gaps	

Qy	6	WLLSLVAVTAQAQTIERQAKTFLDKFNHRAEDLFYOSSLASWYNNTNITEENVQNNA 65
Dd	16	WLPHGLSGMNGSCASVLE-ARRFELENQRRHFEEFLSGNYNTNVTEARQAMIEV 74
Qy	66	GDKSAFLKEOSTLAQMYPLOEQIONLVTKVLQALQONGSSVLSDESKRLNTILANTMS 125
Dd	75	YARNAELNKRLAQOIKSDYVOSEDAIRQAEHLKLGASALNADDYLALQNAISMOT 134
Qy	126	IYSTGKVCNPDPNOEC-LLLEPGLINEIMANSLDYNERLAWESWRSEVGQLRPLYEYV 184
Dd	135	NVATATCVSYTNRSDCSLTLEPHIQERLSHRPAELAWYREWHDKSGCTPMQRNAEYV 194
Qy	185	VLKEMARANIHYDYGWGRGDVEVNGVDGYDSRGOLIEDVHTTEETKPLYEHLHAVY 244
Dd	195	RLTRKASQLNGHSRYADYWVQFYE-----DPDFER-----QLDATEFKLLPYLRQLHGYY 244
Qy	245	RAKLMNAY-PSYISPIGCLPAHLIGDMWGREFWNLYSLTPFGCKPNIDVTDAMVDAMD 303
Dd	245	RFRLRQHYPGVDPVAEGNIPIFSLGNMGOSWNEILDLPPTYPEKFPVDVKAMEKOGYT 304
Qy	304	AQRIFKAEEKFFYSVGLPNNMTQGFWSMLTDFGNQKAVCHPTAWDLGK-GDFRLTMCT 362
Dd	305	VQKLFEI:GGQFFQSGLMRALPPSEFWNLVLTTPDD-RQVVCHASAMDFYQDSVRIMKCT 363
Qy	363	KVTMDDFLTAHHENGHIQYDMAYAAQPFLRNAGANGFHVACGEISLSAATPKHLKSTG 422
Dd	364	EVDSHYFVYVHHEIGHIQQYLYEQQPAVYRGAPNPFGEHAGVDVALSVMSAKHLKAIG 423
Qy	423	LISPDEFDETETENFLKQALTIVGTLPPTYMLEKRWVMVFKEIPKDQMKKKWMEKR 482
Dd	424	LIE-NGRLDEKSRINOLFQALKSKIYFLPGYADVRYRAYVFNELDESQWNCGGFQWMS 482
Qy	483	EIVGVVEPVHDFTYCDPASLFHVSNDYSFIYRTTLTYQFOQEALCQAAKHGEP---- 538
Dd	483	EFGGVPEVPFTEKDFOPPAKYHIDADVELYRYFAAHITQFOFHKVLCKAGQYAPNNSR 542
Qy	539	--LHKCDISNSTAGQKLFNWLRLGKSEPTLALENVVGAKNMVRLPLNYTEPFLTWK 596
Dd	543	LTLDNCDFIGSKAAGRSLSOFLSKGNSRHWEKVLEEFTGETEMDPAALLEYFEPLYQWLK 602
Qy	597	DQKNKSFPVGNSTOWSP 612
Dd	603	QE--NSRLGVPLGWGP 616

RESULT 14	
Q9VLJ6	PRELIMINARY; PRT; 630 AA.
ID	Q9VLJ6
AC	Q9VLJ6;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-DEC-2000 (TrEMBLrel. 19, Last annotation update)

ACER PROTEIN (LD28328P).

GN OR CG10593.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

ON NCBI_TaxID=7227;

RX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,

RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimell B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

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RT Science 287:2185-2195(2000).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=Y, CN BW SP;

RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF003621; AAF52693.1;

DR EMBL: AY051750; AAK93174.1;

DR MEROPS: M02.002;

DR Flybase: FBgn0016122; Acer.

DR InterPro: IPR001548; Peptidase_M2.

DR InterPro: IPR000130; Zn_MTPeptidase.

DR Pfam: PF01401; Peptidase_M2; 1.

DR PRINTS: PR00791; PEPDIPASEA.

DR ProDom: PD004184; Peptidase_M2; 1.

DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.

SQ SEQUENCE 630 AA; 73057 MW; 6D9355EB57773289 CRC64;

Query Match

Best Local Similarity 35.0%; Score 1028; DB 5; Length 630;

Matches 219; Conservative 112; Mismatches 261; Indels 24; Gaps 10;

QY 6 WLLSLVAVTAQSTIEEQAKTFLDKFNHEAEDLFYOSSLASWNYNTNTTEENVOMNNA 65
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 Db 16 WLPGLSMGSCSASVLE-ARRFFELENEQLRRRFFHEELSGYNTVNTVEANQAMIEV 74
 :
 QY 66 GDKWSAFLEKQSTLAQMYPLQETQNTVLKQLAALQONGSSVLSEKSKRLNTILNTMST 125
 :
 Db 75 YARNAELNKLAAQIKSSDYVQSEDADIRQAEBHLKLGASALNADDYALALQNAISSMOT 134
 :
 QY 126 IYSTGKVCNPDNPOEC-LLLEPGLNEMANSLDYNERLAWESWRSEVGKQLRPLVEEVY 184
 || :
 Db 135 NYATATVCSVTNRSDCSLTLEPHIQERLSRDPAEALAWWRREHDKSGTTPMRQNAEYV 194
 :
 QY 185 VLKNEMARAHYEDYGDYWRGDEVYNGVGYRSRQLIEDVHEHTFEETKPLYEHLHAYV 244
 :
 Db 195 RLTRKASQLNGHRSYADYVQVFE-----DPDFER-----QLDATEKQLLPFYRLHGVY 244
 :
 QY 245 RAKLMNAY-PSYISPTICGLPAHLGLGDMWGFRWNLXSLTVFPGQKPNIDVTDAMVQAWD 303
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 Db 245 RFLRQRHYGPDVMPAEGNIPISLLGNMGOSWNLGLDFTTPEKPFVDVKAEMEKQGYT 304
 :
 QY 304 AQRIFKEAEKFFSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCT 362
 || :
 Db 305 VQKLFELGDOFFQSLGMRALPPSPFWNLVSLTRPDD-RHVVCASAMDFYQDSVRIKMC 363
 :
 QY 363 KVTMDPFLTAHMHGHTQYDMAYAAQPLFRNGANEGFHEAVGEIMSLSATPKHLKSIG 422
 :
 Db 364 EVDSHYVYVHHLGHLYQYEQQPAVYRGAPNFGFHEAVGVDVIALSVMSAKHLKAIG 423
 :
 QY 423 LLSDFQEDNETENFLLKQALITVGLPTYMLEKRWNVFKEIPKDKMCKWEMKR 482
 || :
 Db 424 LIE-NGRLDKSRINLQFKALSKIVLPFGYADKYRAYVFNELDESQWNGCFWQMR 482
 :
 QY 483 EIVGVFVPEHDETCYPASLFHVSNDYSFIRYTYTLYQFQFQALCAQAKHEGP---- 538
 :
 Db 483 EFGGVEPVEKTEKDFDPKAKYHIDADVEYLVFAAHIFQFHKALCRKAGYAPNNSR 542
 :
 QY 539 --LHKCDISNSTEAGKLFNMLRLGKSEPTLALENVVGAKNNVRPLNAYFEPLFTWLK 596
 || :
 Db 543 LTLDCNDFIGSKAAGSLQFLSKGNSRHKRVLEETGETEMDPAALLEYFEPFLYQWLK 602
 :
 QY 597 DONKNSFVGWSTDMSP 612
 :
 Db 603 QE--NSRLGVPGLGWGP 616
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 RESULT 15
 Q9D836 PRELIMINARY; PRT; 249 AA.
 ID Q9D836
 AC Q9D836
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 2010305L05RIK PROTEIN.
 GN 2010305L05RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustinch S., Hill D., Hofmann J., Hume D.A., Kamiya M., Lee N.H.,
RA	Lions P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schenbach C., Saya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitcaker C., Wilming L.,
RA	Yawnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA	Hayashizaki Y.
RT	*Functional annotation of a full-length mouse cDNA collection.*;
RL	Nature 409:685-690(2001).
DR	ENBL: AK008530; BAB25723.1: -.
DR	MGI: 1917258; 2010305L05Rik.
DR	InterPro: IPRO01548; Peptide_M2.
DR	PRODom: PD004184; Peptide_M2; 1.
SQ	SEQUENCE 249 AA; 28379 MW; 19372B2B78AAE921 CRC64;
	Query Match 23.4%; Score 1004; DB 11; Length 249;
	Best Local Similarity 75.1%; Pred. No. 1.3e-65;
	Matches 187; Conservative 31; Mismatches 31; Indels 0; Gaps
QY	557 MLRIKGSEPTWALENVVGAKNNVRPLNYPEPFTWLKDKNKSFGVGSWDSPYADQ 616
Db	1 MLSIGNSEPTWALENVVGARNMDVFLPNYQPLEDWLKEQRNRNSFVGWNTEPSYADQ 60
QY	617 SIKVIRSLKSGALGDKAYENDNDNMYLFRRSSVAYAMRQYFLKYKNOMILFGEEDVRVANLK 676
Db	61 SIKVIRSLKSGALGANAYETNNEMFLFRSSVAYAMRKYPFSIIKNOTVTPLEEDVRVSDLK 120
QY	677 PRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLDINSLEFLGTOPTLGPPNQ 736
Db	121 PRVSFYFVFSPQNVDVIPRSEVEDAIRMSGRINDVFLGDNLSLEFLTGHTTLEPPYQ 180
QY	737 PPVSILVIIVGVGMVIVGWGITVLIFGTGRDRKKNKARSGENPYASIDISKGNPNPGQ 796
Db	181 PPVTIILIIIGVVVALVVGIIILITVGLKGRKKKNETREENSVDSMDIGKGSNAGFQ 240
QY	797 NTDDQVTSF 805
Db	241 NSDDAQTSF 249

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Job time : 74 secs

